

Amendments to the Specification:

Please amend the specification as follows:

Please replace the paragraph starting at page 9, line 27, (paragraph [0052] as published in U.S. 2002/0102569) with the following rewritten paragraph:

[0052] Mammalian variants of the cDNA encoding cancer marker protein were identified using BLAST2 with default parameters and the ZOOSEQ databases (Incyte Genomics). These preferred variants have about 90% identity to SEQ ID NO:2 as shown in the table below. The first column shows the SEQ ID_H for the human cDNA; the second column, the SEQ ID_{VAR} for variant cDNAs; the third column, the clone numbers for the variants; the fourth column, the percent identity to the human cDNA; and the fifth column, the nucleotide alignment (Nt_H) of the human and variant cDNAs.

SEQ ID _H	SEQ ID _{VAR}	Clone No.	Identity	Nt _H Alignment
2		008031_Cf.1	89%	541-1123
2	10	034237_Mm.1	90%	667-1173
2	11	702482342	89%	671-1173